

SNPs marker toolbox for molecular identification of nominal and candidate species of the genus *Paleosuchus*

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Abstract: Recent studies have identified the existence of species complexes in crocodylians, including in the New World Caimaninae. Both species of the genus *Paleosuchus* are species complexes with three or four species subsumed under the *P. palpebrosus* epithet and two under the *P. trigonatus* epithet. From the conservation point of view, it is important to recognize the evolutionary and ecological uniqueness of these lineages, regardless of the taxonomic status they may receive. Candidate species of the genus *Paleosuchus* have not yet been formally described and therefore do not have diagnostic morphological characters that would allow their identification in nature. This problem motivated us to develop a SNP (Single Nucleotide Polymorphisms) toolkit that enables molecular identification of the nominal and candidate species of *Paleosuchus*. For this, a ddRADseq (Double Digest RAD-sequencing) protocol was used to obtain reduced representation genome of 20 *P. palpebrosus* samples, five from each of four lineages (“Amazonia”, “Bolivia”, “Madeira” and “Pantanal”), and five samples of *P. trigonatus*, three from the “Amazon” and two from the “Guyana” lineage. We selected from between 11 and 15 private SNPs for each lineage that unambiguously assign individuals to one of these lineages. Additionally, we selected 11 mutually exclusive private SNPs that unambiguously assign individuals to one of the two species complexes. The use of the toolkit is affordable and fast-to-apply in comparison to other molecular identification methods, and so it will enable a rapid molecular assignment of individuals to the newly identified lineages of the genus, which may be suffering different degrees of threat. Additional applications of this marker set are: the assignment of zoo specimens, pet trade individuals, museum samples, or degraded samples to source lineages; molecular identification seized animal parts (eg. bush meat); and identification of the origin of illegally traded animals or their by-products (forensic genetics).

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